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1 TACTAAAGGG AACAAAAGCT GGAGCTCCAC CGCGGTGGCG GCCGCTCTAG AACTAGTGGA
ATGATTTCCC TTGTTTTCGA CCTCGAGGTG GCGCCACCGC CGGCGAGATC TTGATCACCT
5' UTR

~~~~~  
TCCCCCGGGC TGCAGGAATT CGGCACGAGG AACTTTCTGC CTCGTTTTTT TGCTCCTACT  
AGGGGGCCCCG ACGTCCTTAA GCCGTGCTCC TTGAAAGACG GAGCAAAAAA ACCGAGGATGA  
5' UTR SEQ ID NO: 3  
~~~~~

~~~~~  
M S Q E I V Q S G Q T Y  
GTTTTTCTCT TCCAGTTTCT ACCATGTCGC AAGAAATTGT TCAATCAGGA CAAACCTACA  
CAAAAAGAGA AGGTCAAAGA TGGTACAGCG TTCTTTAACA AGTTAGTCCT GTTTGGATGT  
SEQ ID NO: 3  
~~~~~

I I T N A K S G T V V D L S G E D N K S
TCATCACTAA CGCCAAATCC GGCACAGTTG TTGACCTTTC GGGCGAAGAC AACAAATCTA
AGTAGTGATT GCGGTTTAGG CCGTGTCAAC AACTGGAAG CCCGCTTCTG TTGTTTAGAT

I I G F P K H G G T N Q R W T L N W T G
TTATTGGATT TCCAAGCAT GGAGGAACAA ATCAGAGGTG GACCCTCAAC TGGACAGGGA
AATAACCTAA AGGGTTCGTA CCTCCTTGTT TAGTCTCCAC CTGGGAGTTG ACCTGTCCCT
SEQ ID NO: 5
~~~~~

K S W T F R S V S S E M Y L G L N G S P  
AGAGTTGGAC TTTCCGCTCC GTTCTTCTG AAATGTATCT TGGCCTGAAT GGCTCGCCGT  
TCTCAACCTG AAAGGCGAGG CAAAGAAGAC TTTACATAGA ACCGGACTTA CCGAGCGGCA  
SEQ ID NO: 4 (partial)  
~~~~~

SEQ ID NO: 5
~~~~~

~~~~~  
SEQ ID NO: 6 (partial)
~~~~~

S D G T K L V A V T T P V E W R I W H  
CTGATGGAAC AAAACTGGTA GCCGTGACCA CCCCTGTTGA GTGGCGCATC TGGCACGA  
GACTACCTTG TTTGACCAT CGGCACTGGT GGGGACAAC CACCGCGTAG ACCGTGCT

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FIG. 1

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5' UTR  
~~~~~

START
~~~

M S Q E I

1 GCCTCGTTTT TTTGCTCCTA CTGTTTTTCT CTTCCAGTTT CTACCATGTC GCAAGAAATT  
CGGAGCAAAA AAACGAGGAT GACAAAAAGA GAAGGTCAAA GATGGTACAG CGTTCCTTAA

V Q S G Q T Y I I T N A K S G T V V D L

61 GTTCAATCAG GACAAACCTA CATCATCACT AACGCCAAAT CCGGCACAGT TGTGACCTT  
CAAGTTAGTC CTGTTTGGAT GTAGTAGTGA TTGCGGTTTA GGCCGTGTCA ACAACTGGAA

S G E D N K S I I G F P K H G G T N Q R

121 TCGGGCGAAG ACAACAAATC TATTATTGGA TTTCCCAAGC ATGGAGGAAC AAATCAGAGG  
AGCCCGCTTC TGTGTTTAG ATAATAACCT AAAGGGTTCG TACCTCCTTG TTAGTCTCC

W T L N W T G K S W

181 TGGACCCTCA ACTGGACAGG GAAGAGTTGG A 211  
ACCTGGGAGT TGACCTGTCC CTTCTCAACC T

FIG. 2

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      V D L S G E D N K S I I G F P K H G G
1  TTGTTGACCT TTCGGGCGAA GACAACAAAT CTATTATTGG ATTTCCCAAG CATGGAGGAA
   AACAACTGGA AAGCCCCTT CTGTTGTTTA GATAATAACC TAAAGGGTTC GTACCTCCTT

      T N Q R W T L N W T G K S W T F R S V S
61 CAAATCAGAG GTGGACCCTC AACTGGACAG GGAAGAGTTG GACTTTCCGC TCCGTTTCTT
   GTTTAGTCTC CACCTGGGAG TTGACCTGTC CCTTCTCAAC CTGAAAGGCG AGGCAAAGAA

      S E M Y L G L N G S P S D G T K L V A V
121 CTGAAATGTA TCTTGGCCTG AATGGCTCGC CGTCTGATGG AACAAACTG GTAGCCGTGA
   GACTTTACAT AGAACCGGAC TTACCGAGCG GCAGACTACC TTGTTTTGAC CATCGGCACT

      T T P V E W H I W H D E V D P S T Y R I
181 CCACCCCTGT TGAGTGGCAC ATCTGGCACG ACGAAGTTGA CCCTTCAACT TATCGTATCT
   GGTGGGGACA ACTCACCGTG TAGACCGTGC TGCTTCAACT GGGAAGTTGA ATAGCATAGA

                                           A/G polymorphism
                                           ~
      F V P F T T F N M D L Y A Q G S A A P G
241 TTGTACCTTT CACCACATTC AACATGGACC TCTACGCCCA RGGTAGTGCC GCCCCTGGTA
   AACATGGAAA GTGGTGTAAG TTGTACCTGG AGATGCGGGT YCCATCACGG CGGGGACCAT

                                           T/C polymorphism
                                           ~
      T P I T T W Y T W K G I H Q T W R F E L
301 CGCCTATCAC AACTTGGTAT ACATGGAAGG GYATCCACCA AACGTGGAGG TTTGAACTAG
   GCGGATAGTG TTGAACATA TGTACCTTCC CRTAGGTGGT TTGCACCTCC AAACCTTGATC

      T/G polymorphism
      ~
      STOP
      ~~~

 3' UTR
      ~~~~~
A *
361 CTTAGGKTCA GGTTTCGGAT GTAATTTGTG TGTGTAAATC TTCTTGGACC ATGTTGTGCT
   GAATCCMAGT CCAAAGCCTA CATTAAACAC ACACATTTAG AAGAACCTGG TACAACACGA
                                           3' UTR
      ~~~~~
421 TTTATTGTAC TCCGCTTGTT ATCATTATAC CCACCTATGT TGCAACATCT TTTTGGATCC
 AAATAACATG AGGCGAACAA TAGTAATATG GGTGGATACA ACGTTGTAGA AAAACCTAGG
 PolyA tail
      ~~~~~
3' UTR
~
481 CAAAAAAAAA AAA 493
   GTTTTTTTTT TTT

```

FIG. 3

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START  
~ ~ ~

M S Q E I V Q S G Q T Y I I

1 TCTCTTCCAG TTTCTACCAT GTCGCAAGAA ATTGTTCAAT CAGGACAAAC CTACATCATC  
AGAGAAGGTC AAAGATGGTA CAGCGTTCTT TAACAAGTTA GTCCTGTTTG GATGTAGTAG

T N A K S G T V V D L S G E D N K S I I

61 ACTAACGCCA AATCCGGCAC AGTTGTTGAC CTTTCGGGCG AAGACAACAA ATCTATTATT  
TGATTGCGGT TTAGGCCGTG TCAACAACCTG GAAAGCCCGC TTCTGTTGTT TAGATAATAA

G F P K H G G T N Q R W T L N W T G K S

121 GGATTTCCCA AGCATGGAGG AACAAATCAG AGGTGGACCC TCAACTGGAC AGGGAAGAGT  
CCTAAAGGGT TCGTACCTCC TTGTTTAGTC TCCACCTGGG AGTTGACCTG TCCCTTCTCA

W T F R S V S S E M Y L G L N G S P S D

181 TGGACTTTCC GCTCCGTTTC TTCTGAAATG TATCTTGCC TGAATGGCTC GCCGTCTGAT  
ACCTGAAAGG CGAGGCAAAG AAGACTTTAC ATAGAACCGG ACTTACCGAG CGGCAGACTA

G T K L V A V T T P V E W H I W H D E V

241 GGAACAAAC TGGTAGCCGT GACCACCCCT GTTGAGTGGC ACATCTGGCA CGACGAAGTT  
CCTTGTTTTG ACCATCGGCA CTGGTGGGGA CAACTCACCG TGTAGACCGT GCTGCTTCAA

D P S T Y R I F V P F T T F N M D L Y A

301 GACCCTTCAA CTTATCGTAT CTTTGTACCT TTCACCACAT TCAACATGGA CCTCTACGCC  
CTGGGAAGTT GAATAGCATA GAAACATGGA AAGTGGTGTA AGTTGTACCT GGAGATGCGG

A/G polymorphism C/T polymorphism

~ ~

361 Q G S A A P G T P I T T W Y T W K G I H  
CAAGGTAGTG CCGCCCCTGG TACGCCTATC ACAACTTGGT ATACATGGAA GGCATCCAC  
GTTCCATCAC GCGGGGACC ATGCGGATAG TGTTGAACCA TATGTACCTT CCCGTAGGTG

G/T polymorphism

~

STOP  
~ ~ ~

Q T W R F E L A \*

421 CAAACGTGGA GGTGTGAAC AGCTTAGGGT CAGGTTTCGG ATGTAATTTG T 491  
GTTTGACCT CCAAACCTGA TCGAATCCCA GTCCAAAGCC TACATTAAAC A

FIG. 4

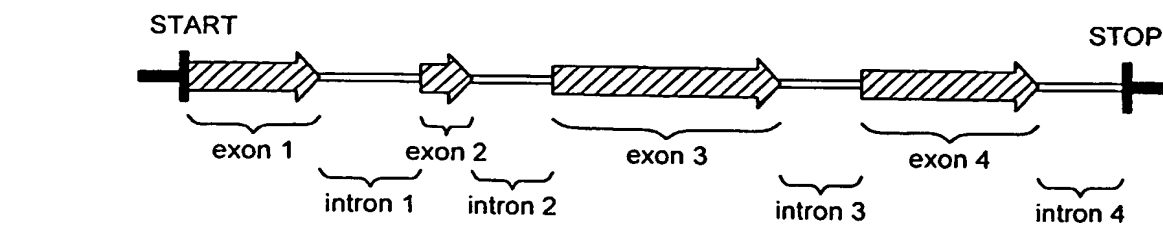


FIG. 5

START  
~ ~ ~

exon 1

1 TCTCTTCCAG TTTCTACCAT GTCGCAAGAA ATTGTTCAAT CAGGACAAAC CTACATCATC  
AGAGAAGGTC AAAGATGGTA CAGCGTTCTT TAACAAGTTA GTCCTGTTTG GATGTAGTAG

exon 1

intron 1

61 T N A K S G T V V D L S G E D N K S  
ACTAACGCCA AATCCGGCAC AGTTGTTGAC CTTTCGGGCG AAGACAACAA ATCTAGTAAG  
TGATTGCGGT TTAGGCCGTG TCAACAACCTG GAAAGCCCCG TTCTGTTGTT TAGATCATTC

intron 1

121 TCGTTTTTAG TCCCATGTTT TTTTTGTCA AAAAAAATTG ACTGACATAT TTTGTCTCCA  
AGCAAAAATC AGGGTACAAA AAAAAACAGT TTTTTTTAAC TGACTGTATA AAACAGAGGT

exon 2

intron 1

intron 2

181 I G F P K H G G T N Q R  
GTTATTGGAT TTCCAAGCA TGGAGGAACA AATCAGAGGG TAGGTCTAGA AATGCACCTC  
CAATAACCTA AAGGGTTCGT ACCTCCTTGT TTAGTCTCCC ATCCAGATCT TTACGTGGAG

exon 3

intron 2

241 W T L N W T G K S  
GTAAATATTG GTTTTTATTG ACATTCATGA ACAGTGGACC CTCAACTGGA CAGGGAAGAG  
CAATTATAAC CAAAAATAAC TGTAAGTACT TGTCACCTGG GAGTTGACCT GTCCCTTCTC

exon 3

301 W T F R S V S S E M Y L G L N G S P S D  
TTGGACTTTC CGCTCCGTTT CTTCTGAAAT GTATCTTGGC CTGAATGGCT CGCCGTCTGA  
AACCTGAAAG GCGAGGCAAA GAAGACTTTA CATAGAACCG GACTTACCGA GCGGCAGACT

exon 3

361 G T K L V A V T T P V E W H I W H D E V  
TGGAACAAAA CTGGTAGCCG TGACCACCCC TGTTGAGTGG CACATCTGGC ACGACGAAGT  
ACCTTGTTTT GACCATCGGC ACTGGTGGGG ACAACTCACC GTGTAGACCG TGCTGCTTCA

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      exon 3                               intron 3
      ~~~~~                               ~~~~~
 D P S T Y
421 TGACCCTTCA ACTTATCGGT GAGTCCCCTA AATATTACTT GCTTGTGGTT CATACTAATA
 ACTGGGAAGT TGAATAGCCA CTCAGGGGAT TTATAATGAA CGAACACCAA GTATGATTAT

 intron 3 exon 4
      ~~~~~                               ~~~~~
      I F V P F T T F N M D L Y A Q G
481  CGTCGTTCGA AGTATCTTTG TACCTTTCAC CACATTCAAC ATGGACCTCT ACGCCCAGGG
      GCAGCAAGCT TCATAGAAAC ATGGAAAGTG GTGTAAGTTG TACCTGGAGA TGCGGGTCCC

      exon 4
      ~~~~~                               ~~~~~
 S A A P G T P I T T W Y T W K G I H Q T
541 TAGTGCCGCC CCTGGTACGC CTATCACAAC TTGGTATACA TGGAAGGGTA TCCACCAAAC
 ATCACGGCGG GGACCATGCG GATAGTGTTG AACCATATGT ACCTTCCCAT AGGTGGTTTG

 intron 4
      ~~~~~                               ~~~~~
      exon 4
      ~~~~~
 W R F E L
601 GTGGAGGTTT GAACTAGGTA GGGCTTGCGA TCTCACCCGG ATCCTCCATG AACTAATGTG
 CACCTCCAAA CTTGATCCAT CCCGAACGCT AGAGTGGGCC TAGGAGGTAC TTGATTACAC

 intron 4 STOP
      ~~~~~
661  ATCACGTCGT GTTCTAGCTT AGGTTTCAGGT TTCGGATGTA ATTTGT      706
      TAGTGCAGCA CAAGATCGAA TCCAAGTCCA AAGCCTACAT TAAACA

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FIG. 6 CONT'D